Nucleotide and Amino Acid Sequence of AIM-I

```
           GGCACGAGCGGCTGCCTGGCTGACTTACAGCAGTCAGACTCTGACAGGTTCATGGCTATG
-51        -+--------+--------+--------+--------+--------+--------     8
           CCGTGCTCGCCGACGGACCGACTGAATGTCGTCAGTCTGAGACTGTCCAAGTACCGATAC
-16                                                               M   A   M    3

           ATGGAGGTCCAGGGGGGGACCCAGCCTGGGACAGACCTGCGTGCTGATCGTGATCTTCACA
 9         -+--------+--------+--------+--------+--------+--------    68
           TACCTCCAGGTCCCCCCCTGGGTCGGACCCTGTCTGGACGCACGACTAGCACTAGAAGTGT
 4         M   E   V   Q   G   G   P   S   L   G   Q   T   C   V   L   I   V   I   F   T    23

           GTGCTCCTGCAGTCTCTCTGTGTGGCTGTAACTTACGTGTACTTTACCAACGAGCTGAAG
69         -+--------+--------+--------+--------+--------+--------   128
           CACGAGGACGTCAGAGAGACACACCGACATTGAATGCACATGAAATGGTTGCTCGACTTC
24         V   L   L   Q   S   L   C   V   A   V   T   Y   V   Y   F   T   N   E   L   K    43

           CAGATGCAGGACAAGTACTCCAAAAGTGGCATTGCTTGTTTCTTAAAAGAAGATGACAGT
129        -+--------+--------+--------+--------+--------+--------   188
           GTCTACGTCCTGTTCATGAGGTTTTCACCGTAACGAACAAAGAATTTTCTTCTACTGTCA
44         Q   M   Q   D   K   Y   S   K   S   G   I   A   C   F   L   K   E   D   D   S    63

           TATTGGGACCCCAATGACGAAGAGAGTATGAACAGCCCCTGCTGGCAAGTCAAGTGGCAA
189        -+--------+--------+--------+--------+--------+--------   248
           ATAACCCTGGGGTTACTGCTTCTCTCATACTTGTCGGGGACGACCGTTCAGTTCACCGTT
64         Y   W   D   P   N   D   E   E   S   M   N   S   P   C   W   Q   V   K   W   Q    83

           CTCCGTCAGCTCGTTAGAAAGATGATTTTGAGAACCTCTGAGGAAACCATTTCTACAGTT
249        -+--------+--------+--------+--------+--------+--------   308
           GAGGCAGTCGAGCAATCTTTCTACTAAAACTCTTGGAGACTCCTTTGGTAAAGATGTCAA
84         L   R   Q   L   V   R   K   M   I   L   R   T   S   E   E   T   I   S   T   V    103

           CAAGAAAAGCAACAAAATATTTCTCCCCTAGTGAGAGAAAGAGGTCCTCAGAGAGTAGCA
309        -+--------+--------+--------+--------+--------+--------   368
           GTTCTTTTCGTTGTTTTATAAAGAGGGGATCACTCTCTTTCTCCAGGAGTCTCTCATCGT
104        Q   E   K   Q   Q   N   I   S   P   L   V   R   E   R   G   P   Q   R   V   A    123

           GCTCACATAACTGGGACCAGAGGAAGAAGCAACACATTGTCTTCTCCAAACTCCAAGAAT
369        -+--------+--------+--------+--------+--------+--------   428
           CGAGTGTATTGACCCTGGTCTCCTTCTTCGTTGTGTAACAGAAGAGGTTTGAGGTTCTTA
124        A   H   I   T   G   T   R   G   R   S   N   T   L   S   S   P   N   S   K   N    143

           GAAAAGGCTCTGGGCCGCAAAATAAACTCCTGGGAATCATCAAGGAGTGGGCATTCATTC
429        -+--------+--------+--------+--------+--------+--------   488
           CTTTTCCGAGACCCGGCGTTTTATTTGAGGACCCTTAGTAGTTCCTCACCCGTAAGTAAG
144        E   K   A   L   G   R   K   I   N   S   W   E   S   S   R   S   G   H   S   F    163
```

FIG.1A

```
        CTGAGCAACTTGCACTTGAGGAATGGTGAACTGGTCATCCATGAAAAAGGGTTTTACTAC
489     -+---------+---------+---------+---------+---------+-------- 548
        GACTCGTTGAACGTGAACTCCTTACCACTTGACCAGTAGGTACTTTTTCCCAAAATGATG
164      L  S  N  L  H  L  R  N  G  E  L  V  I  H  E  K  G  F  Y  Y   183

        ATCTATTCCCAAACATACTTTCGATTTCAGGAGGAAATAAAAGAAAACACAAAGAACGAC
549     -+---------+---------+---------+---------+---------+-------- 608
        TAGATAAGGGTTTGTATGAAAGCTAAAGTCCTCCTTTATTTTCTTTTGTGTTTCTTGCTG
184      I  Y  S  Q  T  Y  F  R  F  Q  E  E  I  K  E  N  T  K  N  D   203

        AAACAAATGGTCCAATATATTTACAAATACACAAGTTATCCTGACCCTATATTGTTGATG
609     -+---------+---------+---------+---------+---------+-------- 668
        TTTGTTTACCAGGTTATATAAATGTTTATGTGTTCAATAGGACTGGGATATAACAACTAC
204      K  Q  M  V  Q  Y  I  Y  K  Y  T  S  Y  P  D  P  I  L  L  M   223

        AAAAGTGCTAGAAATAGTTGTTGGTCTAAAGATGCAGAATATGGACTCTATTCCATCTAT
669     -+---------+---------+---------+---------+---------+-------- 728
        TTTTCACGATCTTTATCAACAACCAGATTTCTACGTCTTATACCTGAGATAAGGTAGATA
224      K  S  A  R  N  S  C  W  S  K  D  A  E  Y  G  L  Y  S  I  Y   243

        CAAGGGGGAATATTTGAGCTTAAGGAAAATGACAGAATTTTTGTTTCTGTAACAAATGAG
729     -+---------+---------+---------+---------+---------+-------- 788
        GTTCCCCCTTATAAACTCGAATTCCTTTTACTGTCTTAAAAACAAAGACATTGTTTACTC
244      Q  G  G  I  F  E  L  K  E  N  D  R  I  F  V  S  V  T  N  E   263

        CACTTGATAGACATGGACCATGAAGCCAGTTTTTTCGGGGCCTTTTTAGTTGGCTAACTG
789     -+---------+---------+---------+---------+---------+-------- 848
        GTGAACTATCTGTACCTGGTACTTCGGTCAAAAAAGCCCCGGAAAAATCAACCGATTGAC
264      H  L  I  D  M  D  H  E  A  S  F  F  G  A  F  L  V  G        281

        ACCTGGAAAGAAAAAGCAATAACCTCAAAGTGACTATTCAGTTTTCAGGATGATACACTA
849     -+---------+---------+---------+---------+---------+-------- 908
        TGGACCTTTCTTTTTCGTTATTGGAGTTTCACTGATAAGTCAAAAGTCCTACTATGTGAT

        TGAAGATGTTTCAAAAAATCTGACCAAAACAAACAAACAGAAAACAGAAAACAAAAAAAC
909     -+---------+---------+---------+---------+---------+-------- 968
        ACTTCTACAAAGTTTTTTAGACTGGTTTTGTTTGTTTGTCTTTTGTCTTTTGTTTTTTTG

        CTCTATGCAATCTGAGTAGAGCAGCCACAACCAAAAAATTCTACAACACACACTGTTCTG
969     -+---------+---------+---------+---------+---------+-------- 1028
        GAGATACGTTAGACTCATCTCGTCGGTGTTGGTTTTTTAAGATGTTGTGTGTGACAAGAC

        AAAGTGACTCACTTATCCCAAGAAAATGAAATTGCTGAAAGATCTTTCAGGACTCTACCT
1029    -+---------+---------+---------+---------+---------+-------- 1088
        TTTCACTGAGTGAATAGGGTTCTTTTACTTTAACGACTTTCTAGAAAGTCCTGAGATGGA

        CATATCAGTTTGCTAGCAGAAATCTAGAAGACTGTCAGCTTCCAAACATTAATGCAATGG
1089    -+---------+---------+---------+---------+---------+-------- 1148
        GTATAGTCAAACGATCGTCTTTAGATCTTCTGACAGTCGAAGGTTTGTAATTACGTTACC
```

FIG.1B

```
      TTAACATCTTCTGTCTTTATAATCTACTCCTTGTAAAGACTGTAGAAGAAAGCGCAACAA
1149  -+---------+---------+---------+---------+---------+--------  1208
      AATTGTAGAAGACAGAAATATTAGATGAGGAACATTTCTGACATCTTCTTTCGCGTTGTT

      TCCATCTCTCAAGTAGTGTATCACAGTAGTAGCCTCCAGGTTTCCTTAAGGGACAACATC
1209  -+---------+---------+---------+---------+---------+--------  1268
      AGGTAGAGAGTTCATCACATAGTGTCATCATCGGAGGTCCAAAGGAATTCCCTGTTGTAG

      CTTAAGTCAAAAGAGAGAAGAGGCACCACTAAAAGATCGCAGTTTGCCTGGTGCAGTGGC
1269  -+---------+---------+---------+---------+---------+--------  1328
      GAATTCAGTTTTCTCTCTTCTCCGTGGTGATTTTCTAGCGTCAAACGGACCACGTCACCG

      TCACACCTGTAATCCCAACATTTTGGGAACCCAAGGTGGGTAGATCACGAGATCAAGAGA
1329  -+---------+---------+---------+---------+---------+--------  1388
      AGTGTGGACATTAGGGTTGTAAAACCCTTGGGTTCCACCCATCTAGTGCTCTAGTTCTCT

      TCAAGACCATAGTGACCAACATAGTGAAACCCCATCTCTACTGAAAGTGCAAAAATTAGC
1389  -+---------+---------+---------+---------+---------+--------  1448
      AGTTCTGGTATCACTGGTTGTATCACTTTGGGGTAGAGATGACTTTCACGTTTTTAATCG

      TGGGTGTGTTGGCACATGCCTGTAGTCCCAGCTACTTGAGAGGCTGAGGCAGGAGAATCG
1449  -+---------+---------+---------+---------+---------+--------  1508
      ACCCACACAACCGTGTACGGACATCAGGGTCGATGAACTCTCCGACTCCGTCCTCTTAGC

      TTTGAACCCGGGAGGCAGAGGTTGCAGTGTGGTGAGATCATGCCACTACACTCCAGCCTG
1509  -+---------+---------+---------+---------+---------+--------  1568
      AAACTTGGGCCCTCCGTCTCCAACGTCACACCACTCTAGTACGGTGATGTGAGGTCGGAC

      GCGACAGAGCGAGACTTGGTTTC
1569  -+---------+---------+-  1591
      CGCTGTCTCGCTCTGAACCAAAG
```

FIG.1C

Alignment of AIM-I to Human Fas Ligand
(Similarity = 48.594 %   Identity = 22.892 %)

4 MEVQGGPSLGQTCVLIVIFTVL................LQSLCVAVTYV 36
   :: ::...::...:.. | : |.. ..:....
15 vdssasspwappgtvlpcptsvprrpgqrrppppppppplppppppppplp 64

37 YFTNELKQMQDKYSKSGIACFLKEDDSYWDPNDEESMNSPCWQVKWQLRQ 86
   ::. |..:..: ..|. |:| :   . ::. .:| ::|..
65 plp..lpplkkrgnhstglcllvm..ffmvlvalvglglgmfql.fhlqk 109

87 LVRKMILRTSEETISTVQEKQQNISPLVRERGPQRVAAHITGTRGRSNTL 136
   : .: .||: ... ||| . .. ..|: . | .||:| |:||.
110 elaelrestsqmhtasslekqighpspppekkelrkvahlt...gksnsr 156

137 SSPNSKNEKALGRKINSWESSRSGHSFLSNLHLRNGELVIHEKGFYYIYS 186
    | | ..:::. | :||.:...:.|:|||:|.|:|::||
157 smplewedty............givllsgvkykkgglvinetglyfvys 193

187 QTYFRFQEEIKENTKNDKQMVQYIYKYTS.YPDPILLMKSARNSCWSKDA 235
    ..||| :.. |: .: : :|. .| ||:.::|.: . |: ...:.
194 kvyfr......gqscnnlplshkvymrnskypqdlvmmegkmmsycttgq 237

236 EYGLYSIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLV 280
    :: | | |::|:|...|:::|.|.: |::::...||| : :
238 mwar.ssylgavfnltsadhlyvnvselslvnfeesqtffglykl 281

FIG.2

Alignment Report of AIM-I, hFas Ligand, TNF-α and TNF-β
by Clustal Method with PAM250 Residue Weight Table

```
                     10              20            30
  1  M A M M E V Q G G P S L - - - - - G Q T C V L I V I F T V L   AIM 1
  1  M Q Q P M N Y P C P Q I F W V D S S A T S S W A P P G S V F   FAS LIGAND
  1  M - - - - - - - - - - - - - - - - - - - - - - - - - - - -   tnfa.pep
  1  M - - - - - - - - - - - - - - - - - - - T P P E R L F       tnfb.pep

                     40              50            60
 26  L Q S L C V A V T Y V Y F T N E L K Q M Q D K Y S K S G I A   AIM 1
 31  P C P S C G P R G - - - - P D Q R R P P P P P P P V S P L P   FAS LIGAND
  2  - - - - - - - - - - - - - - - - - - - - S T E S M I R D V E   tnfa.pep
  9  L P R V C G T T - - - - - - - - - - - - - - - - - - - -     tnfb.pep

                     70              80            90
 56  C F L K E D D S Y W D P N D E E S M N S P C W Q V K W Q L R   AIM 1
 57  - - P P S Q P L P L P P P L T P L K K K D H N T N L W L P V V   FAS LIGAND
 12  - - L A E E A L P - - - - - - - - K K T G G P Q G S R R C L   tnfa.pep
 17  - - - - - - - - - - - - - - - - - - - - - - - L W L L       tnfb.pep

                    100             110           120
 86  Q L V R K M I L R T S E E T I S T V Q E K Q Q N I S P L V R   AIM 1
 85  F F M V L V A L V G M G L G - M Y Q L F H L Q K E L A E L R   FAS LIGAND
 32  F L S L F S F L I V A G A T T L F C L L H F G V I G P Q R E   tnfa.pep
 21  L L G L L L V L - - - - - - - - - - - - - - L P G A Q       tnfb.pep

                    130             140           150
116  E K G P Q R V A A H I T G T R G R S N T L S S P N S K N E K   AIM 1
114  E F T - N Q S L K V S S F E K Q I A N P S T P S E K K E P R   FAS LIGAND
 62  E S P R D L S L I S P L A Q A V R S S S R T P S D - - - - K   tnfa.pep
 34  G L P - G V G L T P S A A Q T A R Q H P K M H L A H S T L K   tnfb.pep

                    160             170           180
146  A L G R K I N S - - - - - - - - W E S S R S G H S F L S N     AIM 1
143  S V A H L T G N P H S R S I P L E W E D T Y G T A L I - S G   FAS LIGAND
 88  P V A H V V A N P Q A E G Q - L Q W L N R R A N A L L A N G   tnfa.pep
 63  P A A H L I G D P - S K Q N S L L W R A N T D R A F L Q D C   tnfb.pep
```

FIG.3A

```
                        190              200             210
167  L H L R N G K L V I H E K G F Y Y I Y S Q T Y F R F Q E E I   AIM 1
172  V K Y K K G G L V I N E T G L Y F V Y S K V Y F R G Q S C N   FAS LIGAND
117  V E L R D N Q L V V P S E G L Y L I Y S Q V L F K G Q S C -   tnfa.pep
92   F S L S N N S L L V P T S G I Y F V Y S Q V V F S C K A Y S   tnfb.pep

                        220              230             240
197  K E N T K N D K Q M V Q Y I Y K Y T S - Y P D P I L L M K S   AIM 1
202  N Q P - - - - - - L N H K V Y M R N S K Y P E D L V L M E E   FAS LIGAND
146  - - - P S T H V L L T H T I S R I A V S Y Q T K V N L L S A   tnfa.pep
122  P K A P S S P L Y L A H E V Q L F S S Q Y P F H V P L L S S   tnfb.pep

                        250              260             270
226  A R N S C W S K D A E Y G L - - - - - Y S I Y Q G G I F E L   AIM 1
226  K R L N Y C - - - - - - T T G Q I W A H S S Y L G A V F N L   FAS LIGAND
173  I K S P C Q R E T P E G A E A K P W Y E P I Y L G C V F Q L   tnfa.pep
152  Q K M V Y P - - - - - G L Q E P W L H S M Y H G A A F Q L   tnfb.pep

                        280              290             300
251  K E N D R I F V S V T N E H L I D K D H E A S - F F G A F L   AIM 1
250  T S A D H L Y V N I S Q L S L I N F E E S - K T F F G L Y -   FAS LIGAND
203  E K G D R L S A E I N R P D Y L D F A E S G Q V Y F G I I -   tnfa.pep
176  T Q G D Q L S T R T D G I P H L V L S P S - T V F F G A F -   tnfb.pep


280  V G -      AIM 1
278  - K L      FAS LIGAND
232  - A L      tnfa.pep
204  - A L      tnfb.pep
```

Decoration 'Decoration #1': Box residues that match the
Consensus within 2 distance units.

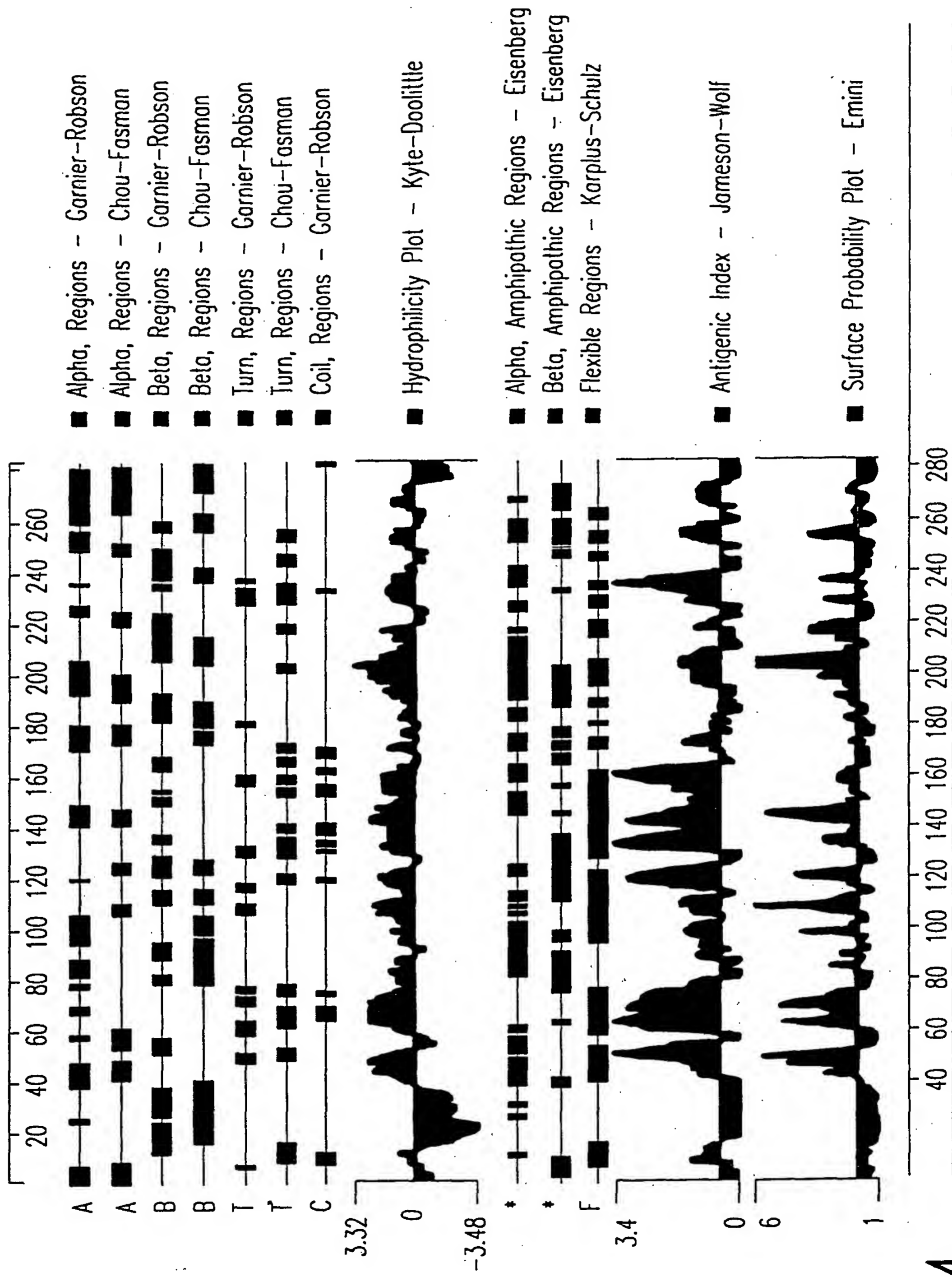# FIG.3B

REGIONAL ANALYSIS OF AIM-I PROTEIN

■ Alpha, Regions — Garnier–Robson
■ Alpha, Regions — Chou–Fasman
■ Beta, Regions — Garnier–Robson
■ Beta, Regions — Chou–Fasman
■ Turn, Regions — Garnier–Robson
■ Turn, Regions — Chou–Fasman
■ Coil, Regions — Garnier–Robson

■ Hydrophilicity Plot — Kyte–Doolittle

■ Alpha, Amphipathic Regions — Eisenberg
■ Beta, Amphipathic Regions — Eisenberg
■ Flexible Regions — Karplus–Schulz

■ Antigenic Index — Jameson–Wolf

■ Surface Probability Plot — Emini

FIG.4